

**IN THE CLAIM**

Please amend claims 1, 3, 5, 7, 15-18, 20, 22, 24 and 26 and cancel claim 25 without disclaiming its subject matter to read as follows:.

1           1. (Currently Amended) A method for determining gender from a human DNA sample,  
2           said method comprising:

3           providing a human DNA sample, said DNA sample containing X chromosomal material  
4           and potentially containing Y chromosomal material;

5           ~~selecting at least one locus from a non combining X-Y homologous region, said region~~  
6           ~~containing a monomorphic *Alu* insertion in one of the X chromosome and the Y chromosome;~~

7           amplifying ~~the selected locus~~ at least one locus containing one of *AluSTYa* locus and  
8           *AluSTXa* locus of the DNA sample in an amplification reaction, wherein the product of the  
9           reaction is a mixture of amplified alleles from the amplified locus present in the sample; and

10          determining the gender of the DNA sample by evaluating the amplified alleles in terms of  
11          size and number.

1           2. (Original) The method of claim 1, wherein said amplification reaction is a polymerase  
2           chain reaction.

1           3. (Currently Amended) The process of claim 2, wherein ~~the amplification step~~  
2           ~~comprises an amplification of~~ said at least one locus is ~~[[an]]~~ *AluSTYa* locus.

1           4. (Original) The method of claim 3, wherein said amplification step comprises the step  
2 of using primer pairs containing the following sequences:

3           Forward 5'- CATGTATTTGATGGGGATAGAGG -3' (SEQ ID NO: 1)

4           and

5           Reverse 5'- CCTTTTCATCCAACCTACCACTGA -3' (SEQ ID NO: 2).

1           5. (Currently Amended) The process of claim 2, wherein ~~the amplification step~~  
2 ~~comprises an amplification of~~ said at least one locus is ~~[[an]]~~ *AluSTXa* locus.

1           6. (Original) The method of claim 5, wherein said amplification step comprises the step  
2 of using primer pairs containing the following sequences:

3           Forward 5'- TGAAGAAATTCAGTTCATAGCTTGT -3' (SEQ ID NO: 3)

4           and

5           Reverse 5'- CAGGAGATCCTGAGATTATGTGG -3' (SEQ ID NO: 4).

1           7. (Currently Amended) The process of claim 2, wherein said amplification step  
2 comprises an amplification of ~~[[an]]~~ *AluSTXa* locus and an amplification of ~~[[an]]~~ *AluSTYa*.

1           8. (Original) The method of claim 7, wherein said amplification step comprises the step  
2 of using primer pairs containing the following sequences:

3 for said amplification of the *AluSTXa* locus, 5'- TGAAGAAATTCAGTTCATAGCTTGT  
4 -3' (SEQ ID NO: 3) and 5'- CAGGAGATCCTGAGATTATGTGG -3' (SEQ ID NO: 4); and  
5 for said amplification of the *AluSTYa*, 5'- CATGTATTTGATGGGGATAGAGG -3'  
6 (SEQ ID NO: 1) and 5'- CCTTTTCATCCAACCTACCACTGA -3' (SEQ ID NO: 2).

1 9. (Original) The method of claim 2, wherein at least one primer of each pair has a  
2 fluorescent label covalently attached thereto.

1 10. (Original) The method of claim 1, wherein the sizes of the amplified alleles are  
2 evaluated by fragment resolution on an agarose gel.

1 11. (Original) The method of claim 10, wherein the sizes of the amplified alleles are  
2 evaluated by comparison with a size standard such that:

3 for a Y insertion *AluSTYa* an *Alu* filled site for Y chromosome has size approximately  
4 528 base pairs and an empty site for X chromosome has size approximately 199 base pairs; or

5 for an X insertion *AluSTXa* an *Alu* filled site for X chromosome has size approximately  
6 878 base pairs and an empty site for Y chromosome has size approximately 556 base pairs.

1 12. (Original) The method of claim 1, wherein male gender is characterized by presence  
2 of two DNA fragments and female gender is characterized by presence of one DNA fragment,  
3 for amplified loci.

1           13. (Withdrawn) A primer pair adapted for assaying a Y insertion in a sex determination  
2 of human cells, each primer pair having the sequence selected from, or constituting a subset of,  
3 the group consisting of:

4           Forward 5'- CATGTATTTGATGGGGATAGAGG -3' (SEQ ID NO: 1)

5           and

6           Reverse 5'- CCTTTTCATCCAACTACCACTGA -3' (SEQ ID NO: 2).

1           14. (Withdrawn) A primer pair adapted for assaying an X insertion in a sex  
2 determination of human cells, each primer having the sequence selected from, or constituting a  
3 subset of, the group consisting of:

4           Forward 5'- TGAAGAAATTCAGTTCATAGCTTGT -3' (SEQ ID NO: 3)

5           and

6           Reverse 5'- CAGGAGATCCTGAGATTATGTGG -3' (SEQ ID NO: 4).

1           15. (Currently Amended) A kit adapted for analyzing alleles of *AluSTY*a locus on  
2 an Y chromosome, said kit comprising a primer pair, each primer of the primer pair having the  
3 sequence selected from, or constituting a subset of, the group consisting of:

4           Forward 5'- CATGTATTTGATGGGGATAGAGG -3' (SEQ ID NO: 1)

5           and

6           Reverse 5'- CCTTTTCATCCAACTACCACTGA -3' (SEQ ID NO: 2).

1           16. (Currently Amended) A kit adapted for analyzing alleles of *[[an]] AluSTXa* locus on  
2 a X chromosome, said kit comprising a primer pair wherein each primer of the primer pair has  
3 the sequence selected from, or constituting a subset of, the group consisting of:

4           Forward 5'- TGAAGAAATTCAGTTCATAGCTTGT -3' (SEQ ID NO: 3)

5           and

6           Reverse 5'- CAGGAGATCCTGAGATTATGTGG -3' (SEQ ID NO: 4).

1           17. (Currently Amended) A kit for determining gender from a sample, comprising:  
2 polymerase chain reaction ~~regents~~reagents comprising a polymerase and buffer; and  
3 a pair of primers to amplify at least one locus of *AluSTYa* locus and *AluSTXa* locus in a  
4 non-combining X-Y homologous region of the DNA sample, said locus containing a  
5 monomorphic *Alu* insertion.

1           18. (Currently Amended) The kit of claim 17, wherein said at least one locus is *[[an]]*  
2 *AluSTYa* locus.

1           19. (Withdrawn) The kit of claim 18, wherein said primer pairs containing the following  
2 sequences:

3           Forward 5'- CATGTATTTGATGGGGATAGAGG -3' (SEQ ID NO: 1)

4           and

Reverse 5'- CCTTTTCATCCAACTACCACTGA -3' (SEQ ID NO: 2).

20. (Currently Amended) The kit of claim 17, wherein said at least one locus is [[an]]  
*AluSTXa* locus.

21. (Withdrawn) The kit of claim 20, wherein said primer pairs containing the following  
sequences:

Forward 5'- TGAAGAAATTCAGTTCATAGCTTGT -3' (SEQ ID NO: 3)

and

Reverse 5'- CAGGAGATCCTGAGATTATGTGG -3' (SEQ ID NO: 4).

22. (Currently Amended) The kit of claim 17, wherein said at least one locus comprises  
[[an]] *AluSTYa* locus and an *AluSTXa* locus.

23. (Withdrawn) The kit of claim 22, wherein said pair of primers comprises:  
a first primer pair, wherein each primer of the first primer pair has the sequence selected  
from, or constituting a subset of, the group consisting of:

Forward 5'- TGAAGAAATTCAGTTCATAGCTTGT -3' (SEQ ID NO: 3)

and

Reverse 5'- CAGGAGATCCTGAGATTATGTGG -3' (SEQ ID NO: 4); and

7 a second primer pair, wherein each primer of the second primer pair has the sequence  
8 selected from, or constituting a subset of, the group consisting of:

9 Forward 5'- CATGTATTTGATGGGGATAGAGG -3' (SEQ ID NO: 1)

10 and

11 Reverse 5'- CCTTTTCATCCAACCTACCACTGA -3' (SEQ ID NO: 2).

1 24. (Currently Amended) A method for quantitating male DNA in a sample, said method  
2 comprising the steps of:

3 amplifying [[a]] at least one locus of *AluSTYa* and *AluSTXa* in the sample by a  
4 polymerase chain reaction, wherein said locus is in a non-combining X-Y homologous region  
5 and contains a monomorphic *Alu* insertion;

6 detecting the product of the amplified locus; and

7 comparing the detected result with a result of standard male DNA to quantitate DNA in a  
8 sample.

1 25. (Canceled)

1 26. (Currently Amended) The method of ~~claim 25~~ claim 24, wherein said amplification  
2 step comprises the step of using primer pairs containing at least one of the following pair of  
3 sequences:

4 5'- TGAAGAAATTCAGTTCATAGCTTGT -3' (SEQ ID NO: 3) and

- 5 5'- CAGGAGATCCTGAGATTATGTGG -3' (SEQ ID NO: 4); and  
6 5'- CATGTATTTGATGGGGATAGAGG -3' (SEQ ID NO: 1) and  
7 5'- CCTTTTCATCCAACCTACCACTGA -3' (SEQ ID NO: 2).